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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/271,584	03/18/1999	EDUARDO BLUMWALD	4001	4345

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EXAMINER
KUBELIK, ANNE R

ART UNIT	PAPER NUMBER
1638	34

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Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No. 09/271,584	Applicant(s) BLUMWALD ET AL.	
	Examiner Anne R. Kubelik	Art Unit 1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *3 June 2002* .

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-33,48,49 and 53-56* is/are pending in the application.

4a) Of the above claim(s) *15,16,33,48 and 49* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-14,17-32 and 53-56* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *with the specification* is/are: a)☐ accepted or b)☒ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12)☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

13)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☒ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a) ☐ The translation of the foreign language provisional application has been received.

15)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449) Paper No(s) _____ .
4) ☐ Interview Summary (PTO-413) Paper No(s). _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: .

DETAILED ACTION

1. The amendments to claims 1-2, 4-5, 7, 12-13, 27-29, 31, and 53 and the addition of claim 56 requested in Paper No. 24, filed 3 June 2002, have been entered. Claims 1-33, 48-49, and 53-56 are pending. Claims 15-16, 33 and 48-49 are withdrawn from consideration. Claims 1-14, 17-32 and 53-56 are exmained.

2. The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.

3. The disclosure is objected to because of the following informalities: throughout the specification all SEQ ID NOs: are in brackets. The brackets should be deleted to not provide confusion at the time or printing - brackets indicate deleted material.

4. The drawings are objected to for the reasons indicated on the form PTO 948 sent with Paper No. 17. Corrected drawings are required in reply to the Office action to avoid abandonment of the application. The objection to the drawings will not be held in abeyance. See 37 CFR 1.85(a) and MPEP 608.02(b).

5. This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825.

Sequence identifiers are missing from the legend of Figure 2, pg 39, line 6, pg 55, lines 26, 28, and 31, pg 55, lines 13-14 and 28-29 and pg 58, lines 2-3.

Full compliance with the sequence rules is required in response to this Office action. A complete response to this Office action must include both compliance with the sequence rules

and a response to the issues set forth below. Failure to fully comply with both of these requirements in the time period set forth in this Office action will be held to be non-responsive.

Response to Amendment

6. The rejection of claim 1 under 35 U.S.C. 112, first paragraph, as containing subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention is obviated by amendment to delete the phrase "not the sequence having GenBank Accession No. AF007271".

7. The rejection of claims 2-14, 17, 19-20 and 26 under 35 U.S.C. 102(a) as being anticipated by Dante et al (1997, GenBank Accession No. AF007271) is WITHDRAWN as Dante et al teach isolated BAC clone TM021B04 and this clone is excluded from the claimed nucleic acids.

Claim Objections

8. Claims 5, 8, 12 and 17 are objected to under 37 CFR 1.75(c) as being in improper form because a multiple dependent claim should refer to other claims in the alternative only. See MPEP § 608.01(n). For purposes of examination, the claims are treated as though they were solely dependent upon claim1.

9. Claims 4, 6 and 56 are objected to because they have brackets aground "SEQ DI NO:1" - brackets indicate material to be deleted from the claim.

Claim Rejections - 35 USC § 112

10. Claims 1-14, 17-32, and 53-56 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Neither the instant specification nor the originally filed claims appear to provide support for the phrase "wherein said nucleic acid molecule is not the sequence of the gene A_TM021B04.4 or complementary to all of the sequence of the gene A_TM021B04.4" in claims 1, 2, 4, 7 and 53. Pg 21, lines 17-18 of the specification simply provides a comparison of SEQ ID NO:1 to A_TM021B04.4 and does not specifically exclude A_TM021B04.4 from the claimed nucleic acid. Thus, such a phrase constitutes NEW MATTER. In response to this rejection, Applicant is required to point to support for the phrase or to cancel the new matter.

11. Claims 1-14, 17-32 and 53-54 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for nucleic acids that encode SEQ ID NO:2, plants transformed with the nucleic acids, and methods of using them to produce salt tolerance plants, does not reasonably provide enablement for a multitude of nucleic acids encoding any plant PNHX transporter or any plant Na^+/H^+ antiport, that hybridize to SEQ ID NO:1; or that have 30% identity to SEQ ID NO:1, plants cells, plant parts and seeds transformed with the nucleic acids, and methods of using them to produce salt-tolerant plants. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims. The rejection is modified from the rejection set forth in the Office action mailed 3 December, 2001,

as applied to claims 1-14 and 17-32. Applicant's arguments filed 3 June 2002 have been fully considered but they are not persuasive.

The claims are broadly drawn to a multitude of nucleic acids encoding any plant PNHX transporter or any plant Na^+/H^+ antiport, that hybridize to SEQ ID NO:1; or that have 30% identity to SEQ ID NO:1, plants cells, plant parts and seeds transformed with the nucleic acids, and methods of using them to produce salt-tolerant plants.

The instant specification, however, only provides guidance for general guidance for preparation of antibodies to the *Arabidopsis* Na^+/H^+ antiport (example 1); general guidance for identification of homologous sequences from other plants (example 2); general guidance for expression of SEQ ID NOs:1, 3, 17 or 19 in *Arabidopsis* or other plants (examples 3-5 and 10-11); general guidance for expression of SEQ ID NOs:1, 3, 17 or 19 in yeast (example 7), general guidance for characterization of nucleic acids encoding Na^+/H^+ antiports from other plants (example 7), general guidance for biochemical and functional analysis Na^+/H^+ antiports of from *Arabidopsis* and other plants (example 8); and general guidance for use of yeast mutants to identify positive and negative regulators of Na^+/H^+ antiport activity (example 9). The specification also provides guidance for cloning the *Arabidopsis* Na^+/H^+ antiport cDNA (AtNHX1, SEQ ID NO:1, encoding SEQ ID NO:2) by screening a cDNA library with GenBank #T75860 and nested PCR amplification of the partial cDNA that was first isolated (pg 55-56); cloning of the *Arabidopsis* AtNHX2-4 Na^+/H^+ antiport cDNA (SEQ ID NO:3, encoding SEQ ID NO:4, SEQ ID NO:17, encoding SEQ ID NO:18 and SEQ DID NO:19, encoding SEQ ID NO:20, respectively) by PCR amplification based on a BAC sequences with predicted amino acid homology to SEQ ID NO:2 (pg 56-57); Southern and Northern blot analysis using SEQ ID

NO:1 as a probe (pg 57); transformation of Arabidopsis plants with an expression vector comprising SEQ ID NO:1 (pg 57-58), and assessment of salt tolerance of the transgenic plants (pg 18-19).

The instant specification fails to provide guidance for making or isolating nucleic acids encoding any plant PNHX transporter or any plant Na^+/H^+ antiport, that hybridize to SEQ ID NO:1; or that have 30% identity to SEQ ID NO:1, plants cells, plant parts and seeds transformed with the nucleic acids, and methods of using them to produce salt-tolerant plants

The instant specification fails to provide guidance for exact hybridization or amplification conditions and probes/primers to use in isolation of nucleic acids other than SEQ ID NOs:1, 3, 17 and 19. The instant specification also fails to provide guidance for exactly which amino acids to substitute for each amino acid of SEQ ID NO:2.

Making amino acid substitutions in plants is not predictable. Making "conservative" substitutions (*e.g.*, substituting one polar amino acid for another, or one acidic one for another) produce unexpected results. Lazar et al (1988, Mol. Cell. Biol. 8:1247-1252) showed that the "conservative" substitution of glutamic acid for aspartic acid at position 47 reduced biological function of transforming growth factor alpha while "nonconservative" substitutions with alanine or asparagine had no effect (abstract). Similarly, Hill et al (1998, Biochem. Biophys. Res. Comm. 244:573-577) teach that when three histidines that are maintained in ADP-glucose pyrophosphorylase across several species are substituted with the "nonconservative" amino acid glutamine, there is little effect on enzyme activity, while the substitution of one of those histidines with the "conservative" amino acid arginine drastically reduced enzyme activity (see

Table 1). The nucleic acids encoding all these mutated proteins, however, would hybridize under high stringency to the nucleic acids encoding the original protein.

Given the claim breath, unpredictability, and lack of guidance as discussed above, undue experimentation would have been required by one skilled in the art to develop and evaluate PHNX-encoding nucleic acids 30% identity to SEQ ID NO:1 or that hybridize to SEQ ID NO:1 or that encode any PHNX transporter. Making all possible single amino acid substitutions in an 532 amino acid long protein like that encoded by SEQ ID NO:1 would require making and analyzing 19^{532} nucleic acids; these nucleic acids would have 99.8% identity to SEQ ID NO:1. Because nucleic acids with 30% identity to SEQ ID NO:1 could encode proteins with up to 372 amino acid substitutions, many more than 19^{532} nucleic acids would need to be made and analyzed.

As the specification does not describe the transformation of any plant with any nucleic acid other than SEQ ID NO:1, undue trial and error experimentation would be required to screen through the myriad of nucleic acids encompassed by the claims and plants transformed therewith, to identify those with salt tolerance, if such plants are even obtainable.

Given the claim breath, unpredictability in the art, undue experimentation, and lack of guidance in the specification as discussed above, the instant invention is not enabled throughout the full scope of the claims.

Applicant urges that one of ordinary skill in the art could isolate nucleic acids encoding PNHX transporters using the guidance provided by the specification and that the amino acid sequence alignment if AtNHX1-3 of Figure 2b provides guidance for which protein regions are important for Na^+/H^+ transported activity. Applicant urges that one would know that amino

acids 82-107, 147-196 and 256-325 are highly conserved among AtNHX1-3. Applicant urges that Strathman et al teaches methods for identification of functionally related genes by using degenerate primers. Applicant also urges that it would not require undue experimentation to identify nucleic acids that have homology to AtHX1 and test their gene products for the ability to transport Na+/H+ ions and provide increased salt tolerance in a cell. Applicant urges that Bowie et al, Lazar et al, Broun et al and Bork are irrelevant to the instant invention because Figure 2b provides the necessary guidance for making proteins with 17% sequence similarity to SEQ ID NO:1 (response pg 12-15).

This is not found persuasive because Hill et al teach that using sequence comparisons to make amino acid substitutions is highly unpredictable. The specification does not teach exactly which PCR primers will isolate nucleic acids with 30% identity to SEQ ID NO:1. Additionally, it is not clear that the AtNHX:3-4 clones are complete as their lengths differ greatly from SEQ ID NOs:2 and 4, and SEQ ID NO:19 has not sequence similarity with SEQ ID NOs:2 and 4.

12. Claims 1-14, 17-32 and 53-54 remain rejected under 35 U.S.C. 112, first paragraph, as containing subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. The rejection is repeated for the reasons of record as set forth in the Office action mailed 3 December, 2001. Applicant's arguments filed 3 June 2002 have been fully considered but they are not persuasive.

The claims are broadly drawn to a multitude of DNA molecules that encode PNHX transporters, that hybridize to SEQ ID NO:1 or have 30% identity to SEQ ID NO:1. In contrast, the specification only describes a coding sequence from *Arabidopsis* that comprises SEQ ID

NOs:1, 3, 17 and 19. Applicant does not describe other DNA molecules encompassed by the claims, and the structural features that distinguish all such nucleic acids from other nucleic acids and how to distinguish nucleic acids that encode plant Na^+/H^+ transporters from nucleic acids that encode non-plant Na^+/H^+ transporters are not provided.

Hence, Applicant has not, in fact, described DNA molecules that encode PNHX transporters within the full scope of the claims, and the specification fails to provide an adequate written description of the claimed invention.

Therefore, given the lack of written description in the specification with regard to the structural and physical characteristics of the claimed compositions, it is not clear that Applicant was in possession of the genus claimed at the time this application was filed.

See *Univ. of California v. Eli Lilly*, 119 F.3d 1559, 43 USPQ 2d 1398 (Fed. Cir. 1997):

> The name cDNA is not in itself a written description of that DNA; it conveys no distinguishing information concerning its identity. While the example provides a process for obtaining human insulin-encoding cDNA, there is no further information in the patent pertaining to that cDNA's relevant structural or physical characteristics; in other words, it thus does not describe human insulin cDNA .... Accordingly, the specification does not provide a written description of the invention ....

and at pg 1406:

> a generic statement such as "vertebrate insulin cDNA" or "mammalian insulin cDNA," without more, is not an adequate written description of the genus because it does not distinguish the genus from others, except by function. It does not specifically define any of the genes that fall within its definition. It does not define any structural features commonly possessed by members of the genus that distinguish them from others. One skilled in the art therefore cannot, as one can do with a fully described genus, visualize or recognize the identity of the members of the genus. A definition by function, as we have previously indicted, does not suffice to define the genus because it is only an indication of what the genes does, not what it is.

See *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ 2d 1016 at page 1021:

> A gene is a chemical compound, albeit a complex one, and ... conception of a chemical compound requires that the inventor be able to define it so as to distinguish it from other materials .... Conception does not occur unless one has a mental picture of the structure of the chemical or is able to define it by its method of preparation, its physical or chemical properties, or whatever characteristics sufficiently distinguish it. It is not sufficient to define it solely by it principal biological property, *e.g.*, encoding human erythropoietin, because an alleged conception having no more specificity than that is simply a wish to know the identity of any material with that biological property.

Applicant urges that given the factors to be analyzed as described in the Written Description Guidelines, the written description requirement has been met. Applicant urges that there are well established techniques for identifying and analyzing genes, that the nucleic acid and amino acid sequences of AtNHX1-4 have been provided, that Na^+/H^+ transport is the physical and chemical property, that salt tolerance is the functional characteristic and that there is a correlation between structure and function because conserved regions among AtNHX1-4 have been identified by the sequence alignment of Figure 2b (response pg 15-17).

This is not found persuasive because the specification does not teach the sequence of the nucleic acids encoding Na^+/H^+ antiports from any plant other than *Arabidopsis* and does not teach the sequence motifs that allow one to distinguish those that encode Na^+/H^+ antiports from all the nucleic acids with 30% identity to SEQ ID NO:1 or that hybridize to SEQ ID NO:1.

13. Claims 1-14, 17-32 and 53-56 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter that Applicant regards as the invention. Dependent claims are included in the rejection.

Claims 1-2, 4, 7 and 56 are indefinite in their recitation of "having Na^+/H^+ transporter activity". It is not clear if the phrase is intended to modify "polypeptide" or "fragment". By position in the claim it modifies "polypeptide".

Claims 2 and 3 are indefinite in their recitation of "moderate and high stringency hybridiztaion conditions" because the listed conditions do not indicate hybridization ans wash times.

In claim 21, "comprising" should be replaced with --, wherein the plant, plant part, seed, plant cell or progeny thereof comprises--.

Claim 31-32 and 53 are indefinite because they lack agreement between the preamble of the methods and the positive method steps. Methods must be circular; the final step must generate the item the method is intended to produce. For example, the method of producing a transgenic plant that expresses elevated levels of PHNX transporter polypeptide in claim 32 ends in transformation of a plant, when it should end in the production of a transgenic plant that expresses elevated levels of PHNX transporter polypeptide.

In claims 55-56, "comprising" should be replaced with --, wherein the nucleic acid molecule comprises--.

Claim Rejections - 35 USC § 102

14. Claims 1-3, 5-6 and 9-14 are rejected under 35 U.S.C. 102(b) as being clearly anticipated by Brant et al (1997, GenBank Accession No. T51330). The rejection is repeated for the reasons of record as set forth in the Office action mailed 3 December, 2001, as applied to claims 1-14, 17, 19-20 and 26. Applicant's arguments filed 3 June 2002 have been fully considered but they are not persuasive.

Brant et al teach a nucleic acid that encodes a human Na^+/H^+ transporter. This nucleic acid would encode a fragment of a plant Na^+/H^+ transporter, would hybridize to SEQ ID NO:1, and would inherently increase salt tolerance in a cell. It would also comprise a fragment of an AtNHX nucleic acid, and would be the same regardless of source.

Applicant urges that Brant et al teach a nucleic acid that encodes a human Na^+/H^+ transporter (response pg 5-6).

This is not found persuasive because Brant et al teach a nucleic acid that would encode a "fragment of a plant polypeptide having Na^+/H^+ transporter activity". At least one amino acid encoded by the nucleic acid of Brant et al would be a fragment of a plant polypeptide. Note that in the claims as written, "having Na^+/H^+ transporter activity" modifies "polypeptide" not "fragment".

15. Claims 1-3, 5-6 and 9-14 remain rejected under 35 U.S.C. 102(b) as being clearly anticipated by Sumitomo Sieyaku KK (1993, GenBank Accession No. Q51524). The rejection is repeated for the reasons of record as set forth in the Office action mailed 3 December, 2001, as applied to claims 1-14, 17, 19-20 and 26. Applicant's arguments filed 3 June 2002 have been fully considered but they are not persuasive.

Sumitomo Sieyaku KK teach a nucleic acid that encodes a rabbit Na^+/H^+ transporter, that would have at least 17% homology to SEQ ID NO:1, that comprises part of SEQ ID NO:1, and that would increase salt tolerance in a cell (see sequence search results). It would also comprise a fragment of an AtNHX nucleic acid, and would be the same regardless of source.

Applicant urges that Sieyaku teach a nucleic acid that encodes a rabbit Na^+/H^+ transporter (response pg 6).

This is not found persuasive because Sieyaku teach a nucleic acid that would encode a "fragment of a plant polypeptide having Na^+/H^+ transporter activity". At least one amino acid encoded by the nucleic acid of Sieyaku would be a fragment of a plant polypeptide. Note that in

the claims as written, "having Na^+/H^+ transporter activity" modifies "polypeptide" not "fragment".

16. Claims 1-3, 5-6, 8-14, 17-20, 26 and 31 remain rejected under 35 U.S.C. 102(b) as being anticipated by Hahnenberger et al (1996, Proc. Natl. Acad. Sci., USA 93:5031-5036). The rejection is repeated for the reasons of record as set forth in the Office action mailed 3 December, 2001. Applicant's arguments filed 3 June 2002 have been fully considered but they are not persuasive.

Hahnenberger et al teach the yeast Na^+/H^+ transporter *sod2*, which would hybridize to SEQ ID NO:1 or would also comprise a fragment of a nucleic acid encoding an AtNHX or a plant Na^+/H^+ transporter, and its transformation into yeast (pg 5033, left column, paragraph 3, to pg 5034, right column, paragraph 1), and vectors comprising the DNA with the 35S promoter (pg 5031, right column, last paragraph).

Applicant urges that Hahnenberger et al teach the yeast Na^+/H^+ transporter (response pg 7).

This is not found persuasive because Hahnenberger et al teach a nucleic acid that would encode a "fragment of a plant polypeptide having Na^+/H^+ transporter activity". At least one amino acid encoded by the nucleic acid of Hahnenberger et al would be a fragment of a plant polypeptide. Note that in the claims as written, "having Na^+/H^+ transporter activity" modifies "polypeptide" not "fragment".

17. Claims 1-3, 5-6, 8-14, 17-24, 26-28, 30-32 and 53-54 remain rejected under 35 U.S.C. 102(b) as being clearly anticipated by Young et al (WO 91/06651), as stated in the prior Office action for claims 1-14, 17-24, 26-32 and 53-54. The rejection is repeated for the reasons

of record as set forth in the Office action mailed 3 December, 2001, as applied to claims 1-3, 5-14, 17-24, 26-32 and 53-54. Applicant's arguments filed 3 June 2002 have been fully considered but they are not persuasive.

Young et al teach tobacco and *Arabidopsis* plants transformed with a gene encoding the Na^+/H^+ transporter *sod2*, which would hybridize to SEQ ID NO:1 or would also comprise a fragment of an AtNHX nucleic acid, and the resistance of these transgenic plants to LiCl (pg 28, paragraph 3, to pg 35). Young et al also teach that that these plants would be resistant to high sodium concentration (pg 9, paragraph 1). The *sod2* gene would be PNHX transporter because it functions in a plant cell.

Applicant urges that Young et al teach the yeast Na^+/H^+ transporter (response pg 7-8).

This is not found persuasive because Young et al all teach a nucleic acid that would encode a "fragment of a plant polypeptide having Na^+/H^+ transporter activity". At least one amino acid encoded by the nucleic acid Young et al would be a fragment of a plant polypeptide. Note that in the claims as written, "having Na^+/H^+ transporter activity" modifies "polypeptide" not "fragment".

Claim Rejections - 35 USC § 103

18. Claims 1-3, 5-6, 8-14, 17-28, 30-32 and 53-54 remain rejected under 35 U.S.C. 103(a) as being unpatentable over Young et al (WO 91/06651) in view of Gordon-Kamm et al (1990, Plant Cell 2:603-618) , as stated in the prior Office action for claims 1-14, 17-32 and 53-54. The rejection is repeated for the reasons of record as set forth in the Office action mailed 3

December, 2001, as applied to claims 1-3, 5-14, 17-32 and 53-54. Applicant's arguments filed 3 June 2002 have been fully considered but they are not persuasive.

The claims are drawn to plants, including monocots, transformed with a nucleic acid that comprises a fragment of an AtNHX or PHNX nucleic acid, and confers salt tolerance, plants comprising those nucleic acids, and methods for production of those plants.

The teachings of Young et al are discussed above. Young et al do not disclose monocots transformed with that gene.

Gordon-Kamm et al teach transformation and regeneration of maize.

At the time the invention was made, it would have been obvious to one of ordinary skill in the art to modify the method of transforming the *sod2* gene into plants as taught by Young et al, and to transform it into a monocot as described in Gordon-Kamm et al. One of ordinary skill in the art would have been motivated to do so because of the suggestion of Young et al to do so (pg 9, paragraph 1).

Applicant urges that Young et al teach the yeast Na^+/H^+ transporter and that Gordon-Kamm et al does not teach Na^+/H^+ transporters (response pg 8-9).

This is not found persuasive for the reasons detailed above, *i.e.*, that Young et al all teach a nucleic acid that would encode a "fragment of a plant polypeptide having Na^+/H^+ transporter activity". At least one amino acid encoded by the nucleic acid Young et al would be a fragment of a plant polypeptide. Note that in the claims as written, "having Na^+/H^+ transporter activity" modifies "polypeptide" not "fragment".

Response to Arguments

19. Applicant also urges that in the following 9 years isolated a nucleic acid encoding a PNHX transporter. Applicant urges that Munns indicates that there is confusion in the art about methods of identification of genes responsible for salt tolerance. Applicant urges that Young et al shares authors with Hahnenberger et al and in the intervening 6 years no one islated plant equivalenst to sod2. Applicant urges that the presnet invention meets a long sought need and cites the publication by Apse et al in Science, a statement in Chemical & Engineering news, an article by Zhang et al published in Nature Biotechnology, and articles published in the New York Times, Science News, and New scientist.com. Applicant urges that the present invention is not obvious because unexpected results were obtained, *i.e.*, plants tarsformed with AtNHX1 were salt tolerant, as shown in Figure 7 (response pg 9-12).

This is not found persuasive the plants taught by Young et al were also salt tolerant. Additionally, the indefiniteness of the claims means the cited art reads on the instant claims.

In response to Applicant's argument based upon the age of the references, contentions that the reference patents are old are not impressive absent a showing that the art tried and failed to solve the same problem notwithstanding its presumed knowledge of the references. See In re Wright, 569 F.2d 1124, 193 USPQ 332 (CCPA 1977).

Munns could not be considered because it was not sent.

20. Claims 55-56 are free of the prior art, given the failure of the prior art to teach or suggest an isolated nucleic acid of SEQ ID NO:1.

21. Claim 7 is free of the prior art, given the failure of the prior art to teach or suggest an isolated AtNHX nucleic acid.

22. Claim 29 is free of the prior art, given the failure of the prior art to teach or suggest transforming a Na^+/H^+ transporter-encoding nucleic acid into a plant that lacks a functional PHNX gene.

Allowable Subject Matter

23. Claims 55-56 would be allowable if rewritten or amended to overcome the rejection(s) under 35 U.S.C. 112, second paragraph, set forth in this Office action.

Conclusion

24. No claim is allowed.

25. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Anne R. Kubelik, whose telephone number is (703) 308-5059. The examiner can normally be reached Monday through Friday, 8:30 am - 5:00 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Amy Nelson, can be reached at (703) 306-3218. The fax phone numbers for the organization where this application or proceeding is assigned are (703) 872-9306 for regular communications and (703) 872-9307 for After Final communications.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to Customer Service at (703) 308-0198.

Anne R. Kubelik, Ph.D.
November 14, 2002

AMY J. NELSON, PH.D
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600